

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/088,859A
Source: IFWIB
Date Processed by STIC: 2/28/06

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,859A

DATE: 07/28/2006

TIME: 14:32:52

Input Set : A:\Revised Sequence Listing filed 2006-07-26.txt
 Output Set: N:\CRF4\07282006\J088859A.raw

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3 <110> APPLICANT: KATO, Seishi
4     NAGATA, Naoki
5     FUJIMURA, Naoko
6     KOBAYASHI, Midori
7     ITO, Koichi
8     ISHIZUKA, Yoshiko
10 <120> TITLE OF INVENTION: A Method For Producing An Antibody By Gene Immunization
12 <130> FILE REFERENCE: 2002_0400A
14 <140> CURRENT APPLICATION NUMBER: 10/088,859A
15 <141> CURRENT FILING DATE: 2002-05-29
17 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06371
18 <151> PRIOR FILING DATE: 2001-07-24
20 <150> PRIOR APPLICATION NUMBER: PCT2000-222743
21 <151> PRIOR FILING DATE: 2000-07-24
23 <150> PRIOR APPLICATION NUMBER: JP2000-254407
24 <151> PRIOR FILING DATE: 2000-08-24
26 <160> NUMBER OF SEQ ID NOS: 18
28 <170> SOFTWARE: PatentIn version 3.3
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 697
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (151)..(600)
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43 aataaaagtta caacttgaa gagagTTTct gcaagacatg acacAAAGGT gctacgagaa      120
45 aatcaaaacg ctgattaaaa gaagcacGGT atg atg acc aaa cat aaa aag tgt      174
46                               Met Met Thr Lys His Lys Lys Cys
47                               1           5
49 ttt ata att gtt ggt gtt tta ata aca act aat att att act ctg ata      222
50 Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile
51   10          15          20
53 gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att      270
54 Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
55 25          30          35          40
57 ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg      318
58 Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
59   45          50          55
61 aat tca agt aaa tac aac tgt tcc actcaa cat gcc gac cta act ata      366
62 Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
63   60          65          70

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65	att gac aac ata gaa gaa atg aat ttt ctt agg cg ^g tat aaa tgc agt	414
66	Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser	
67	75 80 85	
69	tct gat cac tgg att gga ctg aag atg gca aaa aat cga aca gga caa	462
70	Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln	
71	90 95 100	
73	tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt	510
74	Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser	
75	105 110 115 120	
77	gaa gga tgt gcc tac ctc agc gat gat ggt gca gca aca gct aga tgt	558
78	Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys	
79	125 130 135	
81	tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa	600
82	Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His	
83	140 145	
85	gttaatgtct aagataatgg ggaaaaataga aaataaacatt attaagtcta aaaccagcaa	660
87	agtactttt taattaaaca aagttcgagt ttgtac	697
90	<210> SEQ ID NO: 2	
91	<211> LENGTH: 149	
92	<212> TYPE: PRT	
93	<213> ORGANISM: Homo sapiens	
95	<400> SEQUENCE: 2	
97	Met Met Thr Lys His Lys Lys Cys Phe Ile Ile Val Gly Val Leu Ile	
98	1 5 10 15	
101	Thr Thr Asn Ile Ile Thr Leu Ile Val Lys Leu Thr Arg Asp Ser Gln	
102	20 25 30	
105	Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr	
106	35 40 45	
109	Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser	
110	50 55 60	
113	Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn	
114	65 70 75 80	
117	Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys	
118	85 90 95	
121	Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr	
122	100 105 110	
125	Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp	
126	115 120 125	
129	Asp Gly Ala Ala Thr Ala Arg Cys Tyr Thr Glu Arg Lys Trp Ile Cys	
130	130 135 140	
133	Arg Lys Arg Ile His	
134	145	
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139	<212> TYPE: DNA	
140	<213> ORGANISM: Homo sapiens	
143	<220> FEATURE:	
144	<221> NAME/KEY: CDS	
145	<222> LOCATION: (30)..(503)	

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147 <400> SEQUENCE: 3
 148 cttattgctg gcggcctgag gagcccatc atg gcg acg ccc cct aag cgg cgg 53
 149 Met Ala Thr Pro Pro Lys Arg Arg
 150 1 5
 152 gcg gtg gag gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc 101
 153 Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile
 154 10 15 20
 156 agt gac gtg ctg cag cggtt gac aag gtg ctg gac cat cga gac 149
 157 Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
 158 25 30 35 40
 160 aag gta tat gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att 197
 161 Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
 162 45 50 55
 164 gag cga ctc cag gaa gct aag cac tcg gag tta tat atg cag gtg gat 245
 165 Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp
 166 60 65 70
 168 ttg ggc tgt aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc 293
 169 Leu Gly Cys Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg
 170 75 80 85
 172 atc tat gtg gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca 341 489
 173 Ile Tyr Val Ala Leu Gly Tyr Phe Phe Leu Glu Leu Thr Leu Ala
 174 90 95 100
 176 gaa gct ctc aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc 389
 177 Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
 178 105 110 115 120
 180 agc aac agc ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac 437
 181 Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
 182 125 130 135
 184 atg ttg cta gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca 485
 185 Met Leu Leu Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro
 186 140 145 150
 188 gag aag cct cac cat tga cttttcccc ccatcctcag acattaaaga 533
 189 Glu Lys Pro His His
 190 155
 192 gcctgaatgc ctttg 548
 195 <210> SEQ ID NO: 4
 196 <211> LENGTH: 157
 197 <212> TYPE: PRT
 198 <213> ORGANISM: Homo sapiens
 200 <400> SEQUENCE: 4
 202 Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
 203 1 5 10 15
 206 Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
 207 20 25 30
 210 Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
 211 35 40 45
 214 Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
 215 50 55 60
 218 Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp

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219 65          70          75          80
222 Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
223          85          90          95
226 Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
227          100         105         110
230 Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
231          115         120         125
234 Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
235          130         135         140
238 Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
239 145          150          155
242 <210> SEQ ID NO: 5
243 <211> LENGTH: 30
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Oligonucleotide
250 <400> SEQUENCE: 5
251 ccugatatatct catggcgacg cccccctaaggc
254 <210> SEQ ID NO: 6
255 <211> LENGTH: 30
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Oligonucleotide
262 <400> SEQUENCE: 6
263 cccgatatatct caatggtgag gcttctctgg
266 <210> SEQ ID NO: 7
267 <211> LENGTH: 28
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Oligonucleotide
274 <400> SEQUENCE: 7
275 cccgaattca tggcgacgcc ccctaaggc
278 <210> SEQ ID NO: 8
279 <211> LENGTH: 32
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Oligonucleotide
286 <400> SEQUENCE: 8
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290 <210> SEQ ID NO: 9
291 <211> LENGTH: 1643
292 <212> TYPE: DNA
293 <213> ORGANISM: Homo sapiens
296 <220> FEATURE:
297 <221> NAME/KEY: CDS

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298 <222> LOCATION: (25)..(915)		
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303 1 5		
305 cag cag ctg ggc ctc ctg ggg tgt ctt ggc cat ggc gcc ctg gtg ctg	99	
306 Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu		
307 10 15 20 25		
309 caa ctc ctc tcc ttc atg ctc ttg gct ggg gtc ctg gtg gcc atc ctt	147	
310 Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu		
311 30 35 40		
313 gtc caa gtg tcc aag gtc ccc agc tcc cta agt cag gaa caa tcc gag	195	
314 Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu		
315 45 50 55		
317 caa gac gca atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt	243	
318 Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly		
319 60 65 70		
321 gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc	291	
322 Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr		
323 75 80 85		
325 cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag	339	
326 Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln		
327 90 95 100 105		
329 gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg	387	
330 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu		
331 110 115 120		
333 cca gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cgg ctg	435	
334 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu		
335 125 130 135		
337 aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc	483	
338 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile		
339 140 145 150		
341 tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg cca gag	531	
342 Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu		
343 155 160 165		
345 aaa tcc aag ctg cag gag atc tac cag gag ctg acg gag ctg aag gct	579	
346 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala		
347 170 175 180 185		
349 gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag gag atc tac cag	627	
350 Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln		
351 190 195 200		
353 gag ctg acc cag ctg aag gct gca gtg ggt gag ttg cca gac cag tcc	675	
354 Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser		
355 205 210 215		
357 aag cag cag caa atc tat caa gaa ctg acc gat ttg aag act gca ttt	723	
358 Lys Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe		
359 220 225 230		
361 gaa cgc ctg tgc cgc cac tgt ccc aag gac tgg aca ttc ttc caa gga	771	
362 Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly		

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,14,15,16,17,18

VERIFICATION SUMMARY

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